**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings of claims in the application. Canceled claims have been canceled without prejudice.

**Listing of Claims:**

1-120. (Canceled)

121. (Previously presented) A method of determining interactive characteristics of a sample component comprising:

exposing at least two surface regions, each presenting a different chemical, biochemical, or biological functionality, to a sample;

determining an interaction pattern of the sample with the at least two surface regions on the surface, indicative of an interaction characteristic between at least one component of the sample with the at least two surface regions.

122. (Previously presented) The method according to claim 121, wherein the sample includes at least two components that carry, or are adapted to carry, identical immobilized signaling entities, and/or the determining step is carried out without determining the identity of the at least one component after interaction with the at least two surface regions.

123. (Previously presented) The method according to claim 121, comprising:

presenting at least three surface regions, each exposing a different chemical, biochemical, or biological functionality;

exposing the at least three surface regions to the sample; and

determining an interaction pattern of the sample with the at least three surface regions, indicative of an interaction characteristic between at least two components of the sample with each of the at least three surface regions, preferably wherein each of at least two of the at least three components becomes immobilized at a surface region, indicative of the interaction pattern.

124. (Previously presented) The method according to claim 123, wherein the sample is a first sample, further comprising exposing at least three surface regions, each exposing a different chemical, biochemical, or biological functionality, to a second sample;

determining an interaction pattern of the second sample with the at least three surface regions to which the second sample has been exposed, indicative of an interaction characteristic between at least two components of the second sample with each of the at least three surface regions; and

comparing the interaction pattern of the second sample with the interaction pattern of the first sample.

125. (Previously presented) The method according to claim 124, comprising exposing the second sample to a third sample, prior to exposing the second sample to the at least three surface regions, and comparing the interaction pattern of the second sample to the interaction pattern generated when the second sample has not been pre-exposed to the third sample.

126. (Previously presented) The method according to claim 125, wherein the third sample is a drug or a drug candidate.

127. (Previously presented) The method according to claim 125, wherein the second sample comprises a plurality of different species.

128. (Previously presented) The method according to claim 127, wherein the second sample comprises products of a cDNA library.

129. (Previously presented) The method according to claim 124, wherein:

a) the at least three surface regions to which the first sample is exposed are essentially identical to the at least three surface regions to which the second sample is exposed; or

b) each of the at least three surface regions to which the second sample is exposed is arranged to correspond to one of the at least three surface regions to which the first sample was exposed; or

c) at least one of the first sample and second sample is derived from proteins, known drugs, putative drugs, cell lysates, cDNA libraries or their products, natural products and mixtures thereof, preferably wherein:

i) at least one of the first sample and second sample is a cell lysate from a cell that has been treated with a drug or putative drug; or

ii) the interaction pattern is determined by detecting a signal at or near each of the at least two surface regions, preferably wherein the signal is light emission or electrical; or

d) the interaction pattern is determined by surface plasmon resonance (SPR) or quartz crystal microbalance (QCM).

130. (Previously presented) The method according to claim 121, wherein:

a) the sample is selected from known drugs, putative drugs, cell lysates, cDNA libraries or their products, natural products and mixtures thereof, preferably wherein the sample has been exposed to a drug or putative drug; or

b) the interaction pattern is determined by:

i) detecting a signal at the at least two surface regions, preferably wherein the signal is light emission or electrical; or

ii) QCM or SPR; or

c) said method further comprises comparing the interaction pattern to a library of known interaction patterns; or

d) wherein at least one of the two surface regions presents a protein, nucleic acid, peptide, drug, small molecule or a mixture thereof; or

e) said method further comprises immobilizing a colloid to a component of the sample.

131. (Previously presented) The method according to claim 122, comprising:

exposing at least ten surface regions, each presenting a different chemical, biochemical, or biological functionality to a sample containing at least ten components;

determining an interaction pattern of the sample with the at least ten surface regions, indicative of an interaction characteristic between at least ten components of the sample with the at least ten surface regions;

wherein the at least ten components of the sample carry, or are adapted to carry, identical immobilized signaling entities, and/or the determining step is carried out without determining the identity of at least one of the at least ten components after interaction with the at least two surface regions, preferably wherein the determining step is carried out without determining the identity of any of the at least ten components after interaction with the at least two surface regions.